

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/537,839 A
Source: IFWP
Date Processed by STIC: 08/08/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 08/08/2006

PATENT APPLICATION: US/10/537,839A

TIME: 09:04:22

Input Set : A:\PTO.RJ.TXT

Output Set : N:\CRF4\08082006\J537839A.raw

WITH

3 <110> APPLICANT: Hart, Derek Nigel John
 4 Kato, Masato
 6 <120> TITLE OF INVENTION: DEC-205 (LY 75)/DCL-1 INTERGENIC SPLICE VARIANTS ASSOCIATED
 7 HODGKIN'S DISEASE, AND USES THEREOF
 9 <130> FILE REFERENCE: DAVI257.002APC
 11 <140> CURRENT APPLICATION NUMBER: US 10/537,839A
 12 <141> CURRENT FILING DATE: 2005-06-06
 14 <150> PRIOR APPLICATION NUMBER: PCT/AU03/01634
 15 <151> PRIOR FILING DATE: 2003-12-05
 17 <150> PRIOR APPLICATION NUMBER: AU2002953223
 18 <151> PRIOR FILING DATE: 2002-12-06
 20 <160> NUMBER OF SEQ ID NOS: 32
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 5622
 26 <212> TYPE: DNA
 27 <213> ORGANISM: mammalian
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(5619)
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 37 1 5 10 15
 39 ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct 96
 40 Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala
 41 20 25 30
 43 aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag 144
 44 Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
 45 35 40 45
 47 cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac 192
 48 Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
 49 50 55 60
 51 aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc 240
 52 Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
 53 65 70 75 80
 55 caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga 288
 56 Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
 57 85 90 95
 59 atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac 336
 60 Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
 61 100 105 110
 65 cac tct ctg tac gga gct gcc cgg tac cgg ctg gct ctg aag gat gga 384

(Pg-6)

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70 His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
71      130          135          140
73 tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga      480
74 Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
75 145          150          155          160
77 gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat      528
78 Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
79          165          170          175
81 ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca      576
82 Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
83          180          185          190
85 tgg tgt gcc acc acc tta aat tat gaa tat gac cga aag tgg ggc atc      624
86 Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
87          195          200          205
89 tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag      672
90 Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
91      210          215          220
93 cag ttt gga agt tgc tac caa ttt aat act cag acg gct ctt tct tgg      720
94 Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
95 225          230          235          240
97 aaa gaa gct tat gtt tca tgt cag aat caa gga gct gat tta ctg agc      768
98 Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
99          245          250          255
101 atc aac agt gct gct gaa tta act tac ctt aaa gaa aaa gaa ggc att      816
102 Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
103          260          265          270
105 gct aag att ttc tgg att ggt tta aat cag cta tac tct gct aga ggc      864
106 Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
107          275          280          285
109 tgg gaa tgg tca gac cac aaa cca tta aac ttt ctc aac tgg gat cca      912
110 Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro
111      290          295          300
113 gac agg ccc agt gca cct act ata ggt ggc tcc agc tgt gca aga atg      960
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117 gat gct gag tct ggt ctg tgg cag agc ttt tcc tgt gaa gct caa ctg      1008
118 Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
119          325          330          335
121 ccc tat gtc tgc agg aaa cca tta aat aat aca gtg gag tta aca gat      1056
122 Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
123          340          345          350
125 gtc tgg aca tac tca gat acc cgc tgt gat gca ggc tgg ctg cca aat      1104
126 Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
127          355          360          365
129 aat gga ttt tgc tat ctg ctg gta aat gaa agt aat tcc tgg gat aag      1152
130 Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys

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133	gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat	1200		
134	Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His			
135	385 390 395 400			
137	tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat	1248		
138	Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp			
139	405 410 415			
141	atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act	1296		
142	Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr			
143	420 425 430			
145	tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat	1344		
146	Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp			
147	435 440 445			
149	gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc	1392		
150	Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser			
151	450 455 460			
153	tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa	1440		
154	Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys			
155	465 470 475 480			
157	cta aaa tat gta tgc aag aga aag gga gaa aaa ctg aat gac gca agt	1488		
158	Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser			
159	485 490 495			
161	tct gat aag atg tgt cct cca gat gag ggc tgg aag aga cat gga gaa	1536		
162	Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu			
163	500 505 510			
165	acc tgt tac aag att tat gag gat gag gtc cct ttt gga aca aac tgc	1584		
166	Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys			
167	515 520 525			
169	aat ctg act atc act agc aga ttt gag caa gaa tac cta aat gat ttg	1632		
170	Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu			
171	530 535 540			
173	atg aaa aag tat gat aaa tct cta aga aaa tac ttc tgg act ggc ctg	1680		
174	Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu			
175	545 550 555 560			
179	aga gat gta gat tct tgt gga gag tat aac tgg gca act gtt ggt gga	1728		
180	Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly			
181	565 570 575			
183	aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct	1776		
184	Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala			
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187	tcc ccg ggc ggc tgc gtg gct atg tct act gga aag tct gtt gga aag	1824		
188	Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys			
189	595 600 605			
191	tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag	1872		
192	Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys			
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195	aaa atg agt gga ccc ctt ggg cct gaa gaa gca tcc cct aag cct gat	1920		
196	Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp			
197	625 630 635 640			

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205					660				665					670			
207	gaa	gct	gaa	cga	ttc	tgc	caa	gcc	ctt	gga	gca	cac	ctt	tct	agc	ttc	2064
208	Glu	Ala	Glu	Arg	Phe	Cys	Gln	Ala	Leu	Gly	Ala	His	Leu	Ser	Ser	Phe	
209					675			680					685				
211	agc	cat	gtg	gat	gaa	ata	aag	gaa	ttt	ctt	cac	ttt	tta	acg	gac	cag	2112
212	Ser	His	Val	Asp	Glu	Ile	Lys	Glu	Phe	Leu	His	Phe	Leu	Thr	Asp	Gln	
213					690			695				700					
215	ttc	agt	ggc	cag	cat	tgg	ctg	tgg	att	ggt	ttg	aat	aaa	agg	agc	cca	2160
216	Phe	Ser	Gly	Gln	His	Trp	Leu	Trp	Ile	Gly	Leu	Asn	Lys	Arg	Ser	Pro	
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224	Ile	Ile	Met	Pro	Asn	Glu	Phe	Gln	Gln	Asp	Tyr	Asp	Ile	Arg	Asp	Cys	
225					740				745					750			
227	gct	gct	gtc	aag	gta	ttt	cat	agg	cca	tgg	cga	aga	ggc	tgg	cat	ttc	2304
228	Ala	Ala	Val	Lys	Val	Phe	His	Arg	Pro	Trp	Arg	Arg	Gly	Trp	His	Phe	
229					755			760					765				
231	tat	gat	gat	aga	gaa	ttt	att	tat	ttg	agg	cct	ttt	gct	tgt	gat	aca	2352
232	Tyr	Asp	Asp	Arg	Glu	Phe	Ile	Tyr	Leu	Arg	Pro	Phe	Ala	Cys	Asp	Thr	
233					770			775				780					
235	aaa	ctt	gaa	tgg	gtg	tgc	caa	att	cca	aaa	ggc	cgt	act	cca	aaa	aca	2400
236	Lys	Leu	Glu	Trp	Val	Cys	Gln	Ile	Pro	Lys	Gly	Arg	Thr	Pro	Lys	Thr	
237	785					790				795						800	
239	cca	gac	tgg	tac	aat	cca	gac	cgt	gct	gga	att	cat	gga	cct	cca	ctt	2448
240	Pro	Asp	Trp	Tyr	Asn	Pro	Asp	Arg	Ala	Gly	Ile	His	Gly	Pro	Pro	Leu	
241					805					810					815		
243	ata	att	gaa	gga	agt	gaa	tat	tgg	ttt	ggt	gct	gat	ctt	cac	cta	aac	2496
244	Ile	Ile	Glu	Gly	Ser	Glu	Tyr	Trp	Phe	Val	Ala	Asp	Leu	His	Leu	Asn	
245					820				825					830			
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253					850			855				860					
255	aat	ata	tct	ggt	gat	gga	cag	aag	tgg	tgg	ata	aga	att	agc	gag	tgg	2640
256	Asn	Ile	Ser	Gly	Asp	Gly	Gln	Lys	Trp	Trp	Ile	Arg	Ile	Ser	Glu	Trp	
257	865					870				875						880	
259	cca	ata	gat	gat	cat	ttt	aca	tac	tca	cga	tat	cca	tgg	cac	cgc	ttt	2688
260	Pro	Ile	Asp	Asp	His	Phe	Thr	Tyr	Ser	Arg	Tyr	Pro	Trp	His	Arg	Phe	
261					885					890					895		
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268 Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
269          915          920          925
271 atc tgt gaa aaa tat aat gtt tct tcg tta gag aaa tac agc cca gat      2832
272 Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
273          930          935          940
275 tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat      2880
276 Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
277 945          950          955          960
279 aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca      2928
280 Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala
281          965          970          975
283 agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc      2976
284 Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser
285          980          985          990
287 cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct      3024
288 Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala
289          995          1000          1005
293 act tta tgg att ggt ttg cgc tgg act gcc tat gaa aag ata aac      3069
294 Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn
295          1010          1015          1020
297 aaa tgg aca gat aac aga gag ctg acg tac agt aac ttt cac cca      3114
298 Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro
299          1025          1030          1035
301 tta ttg gtt agt ggg agg ctg aga ata cca gaa aat ttt ttt gag      3159
302 Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu
303          1040          1045          1050
305 gaa gag tct cgc tac cac tgt gcc cta ata ctc aac ctc caa aaa      3204
306 Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys
307          1055          1060          1065
309 tca ccg ttt act ggg acg tgg aat ttt aca tcc tgc agt gaa cgc      3249
310 Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg
311          1070          1075          1080
313 cac ttt gtg tct ctc tgt cag aaa tat tca gaa gtt aaa agc aga      3294
314 His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg
315          1085          1090          1095
317 cag acg ttg cag aat gct tca gaa act gta aag tat cta aat aat      3339
318 Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn
319          1100          1105          1110
321 ctg tac aaa ata atc cca aag act ctg act tgg cac agt gct aaa      3384
322 Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys
323          1115          1120          1125
325 agg gag tgt ctg aaa agt aac atg cag ctg gtg agc atc acg gac      3429
326 Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp
327          1130          1135          1140
329 cct tac cag cag gca ttc ctc agt gtg cag gcg ctc ctt cac aac      3474
330 Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 5,13,142

Seq#:11; Xaa Pos. 5,13,142

Seq#:13; N Pos. 43

VERIFICATION SUMMARY

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L:1830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:48
M:341 Repeated in SeqNo=10
L:1920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:2029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0